SEQUENCE LISTING

<110> PITTMAN, DEBRA D.

<120> COMPOSITIONS AND METHODS FOR TREATING RAGE-ASSOCIATED DISORDERS

<130> WYTH-P01-002

<140> 10/643,589
<141> 2003-08-18

<150> 60/404,205
<151> 2002-08-16

<160> 13

<170> PatentIn version 3.5

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<212> DNA
<213> Mus sp.

<220>
<223> Murine Soluble RAGE_FC

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gcccctaaga agccgcccca gcagctagaa tggaaactga acacaggaag aactgaagct 180

tggaaggtcc tctctcccca gggaggcccc tgggacagcg tggctcaaat cctccccaat 240

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actaacaggc gagggaagga ggtcaagtcc aactaccgag tccgagtcta ccagattcct 360

gggaagccag aaattgtgga tcctgcctct gaactcacag ccagtgtccc taataaggtg 420

gggacatgtg tgtctgaggg aagctaccct gcagggaccc ttagctggca cttagatggg 480

aaacttctga ttcccgatgg caaagaaaca ctcgtgaagg aagagaccag gagacaccct 540

gagacgggac tctttacact gcggtcagag ctgacagtga tccccaccca aggaggaacc 600

acccatccta ccttctcctg cagtttcagc ctgggccttc cccggcgcag acccctgaac 660

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cccagccctg tgctgctcct ccctgaggtg gggcacgcgg atgagggcac ctatagctgc 900

gtggccaccc accctagcca cggacctcag gaaagccctc ctgtcagcat cagggtcaca 960

gaaaccggcg atgaggggcc agctgaaggc tctgtgggtg agtctgggct gggtacgcta 1020

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<223> Murine Soluble RAGE_FC

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        35                  40                  45

Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
    50                  55                  60

Ser Pro Gln Gly Gly Pro Trp Asp Ser Val Ala Gln Ile Leu Pro Asn
65                  70                  75                  80

Gly Ser Leu Leu Leu Pro Ala Thr Gly Ile Val Asp Glu Gly Thr Phe
                85                  90                  95

Arg Cys Arg Ala Thr Asn Arg Arg Gly Lys Glu Val Lys Ser Asn Tyr
            100                 105                 110

Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp Pro
        115                 120                 125

Ala Ser Glu Leu Thr Ala Ser Val Pro Asn Lys Val Gly Thr Cys Val
    130                 135                 140

Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp Gly
145                 150                 155                 160

Lys Leu Leu Ile Pro Asp Gly Lys Glu Thr Leu Val Lys Glu Glu Thr
                165                 170                 175

Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Arg Ser Glu Leu Thr
            180                 185                 190

Val Ile Pro Thr Gln Gly Gly Thr Thr His Pro Thr Phe Ser Cys Ser
        195                 200                 205

Phe Ser Leu Gly Leu Pro Arg Arg Arg Pro Leu Asn Thr Ala Pro Ile
    210                 215                 220

Gln Leu Arg Val Arg Glu Pro Gly Pro Pro Glu Gly Ile Gln Leu Leu
225                 230                 235                 240

Val Glu Pro Glu Gly Gly Ile Val Ala Pro Gly Gly Thr Val Thr Leu
                245                 250                 255
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Thr Cys Ala Ile Ser Ala Gln Pro Pro Pro Gln Val His Trp Ile Lys
260 265 270

Asp Gly Ala Pro Leu Pro Leu Ala Pro Ser Pro Val Leu Leu Leu Pro
275 280 285

Glu Val Gly His Ala Asp Glu Gly Thr Tyr Ser Cys Val Ala Thr His
290 295 300

Pro Ser His Gly Pro Gln Glu Ser Pro Pro Val Ser Ile Arg Val Thr
305 310 315 320

Glu Thr Gly Asp Glu Gly Pro Ala Glu Gly Ser Val Gly Glu Ser Gly
325 330 335

Leu Gly Thr Leu Ala Leu Ala
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<210> 3
<211> 1810
<212> DNA
<213> Mus sp.

<220>
<223> Murine solTNFRII_FC

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cagatctcac aggaatacta tgacaggaag gctcagatgt gctgtgctaa gtgtcctcct 180

ggccaatatg tgaaacattt ctgcaacaag acctcggaca ctgtgtgtgc ggactgtgag 240

gcaagcatgt atacccaggt ctggaaccag tttcgtacat gtttgagctg cagttcttcc 300

tgtagcactg accaggtgga gacccgcgcc tgcactaaac agcagaaccg agtgtgtgct 360

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aggctgagca agtgcggccc tggcttcgga gtggccagtt caagagcccc aaatggaaat 480

gtgctatgca aggcctgtgc cccagggacg ttctctgaca ccacatcatc cacagatgtg 540

tgcaggcccc accgcatctg tagcatcctg gctattcccg gaaatgcaag cacagatgca 600

gtctgtgcgc ccgagtcccc aactctaagt gccatcccaa ggacactcta cgtatctcag 660

ccagagccca caagatccca acccctggat caagagccag ggcccagcca aactccaagc 720

atccttacat cgttgggttc aacccccatt attgaacaaa gtaccaaggg tggcgagccc 780

cgcggaccga caatcaagcc ctgtcctcca tgcaaatgcc caggtaagtc actagaccag 840

agctccactc ccgggagaat ggtaagtgct ataaacatcc ctgcactaga ggataagcca 900

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cttacttcat gtacagcaag ctgagagtgg aaaagaagaa ctgggtggaa agaaatagct 1620

actcctgttc agtggtccac gagggtctgc acaatcacca cacgactaag agcttctccc 1680

ggactccggg taaatgagct cagcacccac aaaactctca ggtccaaaga gacacccaca 1740

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<210> 4
<211> 258
<212> PRT
<213> Mus sp.

<220>
<223> Murine solTNFRII_FC

<400> 4

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Trp	Ala	Thr	Gly	His	Thr	Val	Pro	Ala	Gln	Val	Val	Leu	Thr	Pro	Tyr
			20					25					30		

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Lys Pro Glu Pro Gly Tyr Glu Cys Gln Ile Ser Gln Glu Tyr Tyr Asp
        35                  40                  45

Arg Lys Ala Gln Met Cys Cys Ala Lys Cys Pro Pro Gly Gln Tyr Val
    50                  55                  60

Lys His Phe Cys Asn Lys Thr Ser Asp Thr Val Cys Ala Asp Cys Glu
65                  70                  75                  80

Ala Ser Met Tyr Thr Gln Val Trp Asn Gln Phe Arg Thr Cys Leu Ser
                85                  90                  95

Cys Ser Ser Ser Cys Ser Thr Asp Gln Val Glu Thr Arg Ala Cys Thr
            100                 105                 110

Lys Gln Gln Asn Arg Val Cys Ala Cys Glu Ala Gly Arg Tyr Cys Ala
        115                 120                 125

Leu Lys Thr His Ser Gly Ser Cys Arg Gln Cys Met Arg Leu Ser Lys
    130                 135                 140

Cys Gly Pro Gly Phe Gly Val Ala Ser Ser Arg Ala Pro Asn Gly Asn
145                 150                 155                 160

Val Leu Cys Lys Ala Cys Ala Pro Gly Thr Phe Ser Asp Thr Thr Ser
                165                 170                 175

Ser Thr Asp Val Cys Arg Pro His Arg Ile Cys Ser Ile Leu Ala Ile
            180                 185                 190

Pro Gly Asn Ala Ser Thr Asp Ala Val Cys Ala Pro Glu Ser Pro Thr
        195                 200                 205

Leu Ser Ala Ile Pro Arg Thr Leu Tyr Val Ser Gln Pro Glu Pro Thr
    210                 215                 220

Arg Ser Gln Pro Leu Asp Gln Glu Pro Gly Pro Ser Gln Thr Pro Ser
225                 230                 235                 240

Ile Leu Thr Ser Leu Gly Ser Thr Pro Ile Ile Glu Gln Ser Thr Lys
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Gly Gly
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<210> 5
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Human RAGE-LBE fused to an Fc element

<220>
<221> MOD_RES
<222> (423)..(423)
<223> Any amino acid

<400> 5

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Trp Gly Ala Val Val Gly Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu
            20                  25                  30

Pro Leu Val Leu Lys Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg
        35                  40                  45

Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
    50                  55                  60

Ser Pro Gln Gly Gly Gly Pro Trp Asp Ser Val Ala Arg Val Leu Pro
65                  70                  75                  80

Asn Gly Ser Leu Phe Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Ile
                85                  90                  95

Phe Arg Cys Gln Ala Asn Ile Asn Arg Asn Gly Lys Glu Thr Lys Ser
            100                 105                 110

Asn Tyr Arg Val Arg Val Tyr Gln Ile Pro Glu Lys Pro Glu Ile Val
        115                 120                 125

Asp Ser Ala Ser Glu Leu Thr Ala Gly Val Pro Asn Lys Val Gly Thr
    130                 135                 140

Cys Val Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu
145                 150                 155                 160
```

```
Asp Gly Lys Pro Leu Val Leu Asn Glu Lys Gly Val Ser Val Lys Glu
                165                 170                 175

Gln Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu
            180                 185                 190

Leu Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser
        195                 200                 205

Cys Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala
    210                 215                 220

Pro Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln
225                 230                 235                 240

Leu Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val
                245                 250                 255

Thr Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp
            260                 265                 270

Met Lys Asp Gly Val Pro Leu Pro Leu Pro Pro Ser Pro Val Leu Ile
        275                 280                 285

Leu Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala
    290                 295                 300

Thr His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser
305                 310                 315                 320

Ile Ile Glu Pro Gly Glu Glu Gly Pro Thr Ala Gly Ser Val Gly Gly
                325                 330                 335

Ser Gly Leu Gly Thr Leu Ala Leu Ala Cys Ala Gly Ser Gly Ser Gly
            340                 345                 350

Ser Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
        355                 360                 365

Pro Ala Pro Glu Ala Leu Gly Ala Pro Ser Val Phe Leu Phe Pro Asp
    370                 375                 380

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
385                 390                 395                 400
```

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
405 410 415

Tyr Val Asp Gly Val Glu Xaa Gln Asn Ala Lys Thr Lys Pro Arg Glu
420 425 430

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
435 440 445

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
450 455 460

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
465 470 475 480

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
485 490 495

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
500 505 510

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
515 520 525

Lys Cys Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
530 535 540

Leu Tyr Ser Lys Leu Thr Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
545 550 555 560

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
565 570 575

Lys Ser Leu Ser Leu Ser Pro Gly Lys
580 585

<210> 6
<211> 1761
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Human RAGE-LBE fused to an Fc element

<400> 6

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gcccccaaga aaccacccca gcggctggaa tggaaactga acacaggccg gacagaagct 180

tggaaggtcc tgtctcccca gggaggaggc ccctgggaca gtgtggctcg tgtccttccc 240

aacggctccc tcttccttcc ggctgtcggg atccaggatg aggggatttt ccggtgccag 300

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gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 1320

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<211> 404
<212> PRT
<213> Homo sapiens

<220>
<223> HUMAN RAGE

<400> 7

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Trp	Gly	Ala	Val	Val	Gly	Ala	Gln	Asn	Ile	Thr	Ala	Arg	Ile	Gly	Glu
			20					25					30		
Pro	Leu	Val	Leu	Lys	Cys	Lys	Gly	Ala	Pro	Lys	Lys	Pro	Pro	Gln	Arg
		35					40					45			
Leu	Glu	Trp	Lys	Leu	Asn	Thr	Gly	Arg	Thr	Glu	Ala	Trp	Lys	Val	Leu
	50					55					60				
Ser	Pro	Gln	Gly	Gly	Gly	Pro	Trp	Asp	Ser	Val	Ala	Arg	Val	Leu	Pro
65					70					75					80
Asn	Gly	Ser	Leu	Phe	Leu	Pro	Ala	Val	Gly	Ile	Gln	Asp	Glu	Gly	Ile
				85					90					95	
Phe	Arg	Cys	Gln	Ala	Met	Asn	Arg	Asn	Gly	Lys	Glu	Thr	Lys	Ser	Asn
			100					105					110		
Tyr	Arg	Val	Arg	Val	Tyr	Gln	Ile	Pro	Gly	Lys	Pro	Glu	Ile	Val	Asp
		115					120					125			
Ser	Ala	Ser	Glu	Leu	Thr	Ala	Gly	Val	Pro	Asn	Lys	Val	Gly	Thr	Cys
	130					135					140				
Val	Ser	Glu	Gly	Ser	Tyr	Pro	Ala	Gly	Thr	Leu	Ser	Trp	His	Leu	Asp
145					150					155					160

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Gly Lys Pro Leu Val Pro Asn Glu Lys Gly Val Ser Val Lys Glu Gln
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Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu Leu
            180                 185                 190

Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser Cys
        195                 200                 205

Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala Pro
    210                 215                 220

Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln Leu
225                 230                 235                 240

Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val Thr
                245                 250                 255

Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp Met
            260                 265                 270

Lys Asp Gly Val Pro Leu Pro Leu Pro Pro Ser Pro Val Leu Ile Leu
        275                 280                 285

Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr
    290                 295                 300

His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser Ile
305                 310                 315                 320

Ile Glu Pro Gly Glu Glu Gly Pro Thr Ala Gly Ser Val Gly Gly Ser
                325                 330                 335

Gly Leu Gly Thr Leu Ala Leu Ala Leu Gly Ile Leu Gly Gly Leu Gly
            340                 345                 350

Thr Ala Ala Leu Leu Ile Gly Val Ile Leu Trp Gln Arg Arg Gln Arg
        355                 360                 365

Arg Gly Glu Glu Arg Lys Ala Pro Glu Asn Gln Glu Glu Glu Glu Glu
    370                 375                 380

Arg Ala Glu Leu Asn Gln Ser Glu Glu Pro Glu Ala Gly Glu Ser Ser
385                 390                 395                 400
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Thr Gly Gly Pro

<210> 8
<211> 1436
<212> DNA
<213> Homo sapiens

<220>
<223> HUMAN RAGE

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cacaggccgg acagaagctt ggaaggtcct gtctccccag ggaggaggcc cctgggacag 240

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<210> 9
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<223> N-Terminal Human RAGE Sequence

<400> 9
Met Ala Ala Gly Thr Ala Val Gly Ala Trp Val Leu Val Leu Ser Leu
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Trp Gly Ala Val Val Gly Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu
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Pro Leu Val Leu Lys Cys Lys Gly
35 40

<210> 10
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

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<210> 11
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 11
agaggcagga tccacaattt ctggcttccc aggaat 36

<210> 12
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 12
gactgataat acgactcact atagggcgaa gaggcaggat ccacaatttc tggctt 56

<210> 13
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 13
atgccagcgg ggacagcagc tagagcctgg gtgctggtt 39